

REMARKS

In the Specification:

Amendments to paragraph numbers 0104, 0188, and 0196 were made to correct typographical errors. No new matter has been added. Marked copies of each paragraph delineating each amendment are submitted herewith in a document entitled "VERSION WITH MARKINGS TO SHOW CHANGES MADE".

In the Claims:

Claims 1- 34 have been cancelled and new claims 35-59 have been added. Support for the newly added claims may be found in the application as originally filed.

Specifically, support for new claim 34 may be found in paragraph number 0094, pages 21 to 22, pages 43 to 48, original claim 31, and throughout the application as originally filed.

Support for new claims 35-44 and claims 56 to 59 may be found on pages 69 to 73, Example 7, and throughout the application as originally filed.

Support for new claim 45 and 48 may be found on pages 69 to 70, and throughout the application as originally filed.

Support for new claim 46 and 49 may be found on page 29, Example 8, and throughout the application as originally filed.

Support for new claim 47 and 50 may be found on page 13, pages 62 to 63, and throughout the application as originally filed.

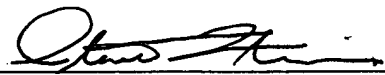
Support for new claim 51-54 may be found on pages 4 to 8, page 10, and throughout the application as originally filed.

No new matter has been added. Applicants believe that all of the pending claims before the Examiner are in condition for allowance. An early Office Action to that effect is, therefore, earnestly solicited.

If any fee is due in connection herewith not already accounted for, please charge such fee to Deposit Account No. 19-3880 of the undersigned. Furthermore, if any extension of time not already accounted for is required, such extension is hereby petitioned for, and it is requested that any fee due for said extension be charged to the above-stated Deposit Account.

Respectfully submitted,

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Date: February 25, 2003



VERSION WITH MARKINGS TO SHOW CHANGES MADE

In the Specification:

On page 28, replace paragraph [0104] with the following paragraph:

[0104] In preferred embodiments, the present invention encompasses a polynucleotide lacking the initiation start codon, in addition to, the resulting encoded polypeptide of HGPRBMY4. Specifically, the present invention encompasses the polynucleotide corresponding to nucleotides 4 through 954 of SEQ ID NO:1, and the polypeptide corresponding to amino acids 2 through 318 of SEQ ID NO:2. Also encompassed are recombinant vectors comprising said encoding sequence, and host cells comprising said vector.

On page 55, replace paragraph [0188] with the following paragraph:

[0188] Asparagine glycosylation sites have the following consensus pattern, N-{P}-[ST]-{P}, wherein N represents the glycosylation site. However, it is well known that that potential N-glycosylation sites are specific to the consensus sequence Asn-Xaa-Ser/Thr. However, the presence of the consensus tripeptide is not sufficient to conclude that an asparagine residue is glycosylated, due to the fact that the folding of the protein plays an important role in the regulation of N-glycosylation. It has been shown that the presence of proline between Asn and Ser/Thr will inhibit N-glycosylation; this has been confirmed by a recent statistical analysis of glycosylation sites, which also shows that about 50% of the sites that have a proline C-terminal to Ser/Thr are not glycosylated. Additional information relating to asparagine glycosylation may be found in reference to the following publications, which are hereby incorporated by reference herein: Marshall R.D., Annu. Rev. Biochem. 41:673-702(1972); Pless D.D., Lennarz W.J., Proc. Natl. Acad. Sci. U.S.A. 74:134-138(1977); Bause E., Biochem. J. 209:331-336(1983); Gavel Y., von Heijne G., Protein Eng. 3:433-442(1990); and Miletich J.P., Broze G.J. Jr., J. Biol. Chem. 265:11397-11404(1990).

On page 58, replace paragraph [0196] with the following paragraph:

[0196] The putative consensus sequence for GPCRs comprises the conserved triplet and also spans the major part of the third transmembrane helix, and is as follows:

[GSTALIVMFYWC]-[GSTANCPDE]-{EDPKRH}-x(2)-[LIVMNQGA]-x(2)-
[LIVMFT]-[GSTANC]-[LIVMFYWSTAC]-[DENH]-R-[FYWCSH]-x(2)-[LIVM],
where "X" represents any amino acid.